

L Number	Hits	Search Text	DB	Time stamp
1	191	urotensin	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/03/10 08:49
2	131449	mammal\$	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/03/10 08:49
3	114	urotensin and mammal\$	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/03/10 08:49
4	39860	hypertens\$	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/03/10 08:49
5	70	(urotensin and mammal\$) and hypertens\$	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/03/10 08:54
6	95	urotensin adj II	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/03/10 08:54
7	61	hypertens\$ and (urotensin adj II)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/03/10 09:05
8	11949	neurodegen\$	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/03/10 09:05
9	39	(urotensin adj II) and neurodegen\$	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/03/10 09:05

(FILE 'HOME' ENTERED AT 09:12:47 ON 10 MAR 2003)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, CANCERLIT' ENTERED AT 09:13:04 ON  
10 MAR 2003

L1 879 S UROTENSIN II  
L2 6 S NEURODGEN?  
L3 52983 S NEURODEGEN?  
L4 1 S L1 AND L3  
L5 2947506 S NEURO?  
L6 379 S L1 AND L5  
L7 7240298 S DISEASE  
L8 236783 S TRAUMA  
L9 37 S L6 AND L7  
L10 1 S L6 AND L8  
L11 31 DUP REM L9 (6 DUPLICATES REMOVED)  
L12 1061050 S ANTAGONIST?  
L13 113 S L1 AND L12  
L14 67 DUP REM L13 (46 DUPLICATES REMOVED)  
L15 5 S L14 NOT PY>1998

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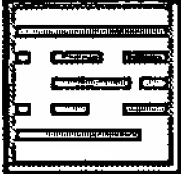
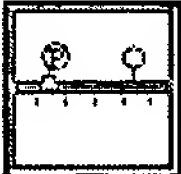
General information about the entry	
Entry name	UR2_MOUSE
Primary accession number	Q9QZQ3
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 40, October 2001
Sequence was last modified in	Release 40, October 2001
Annotations were last modified in	Release 41, February 2003
Name and origin of the protein	
Protein name	Urotensin II [Precursor]
Synonyms	U-II UII
Gene name	UTS2
From	Mus musculus (Mouse) [TaxID: 10090]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
References	
[1] SEQUENCE FROM NUCLEIC ACID. TISSUE=Spinal cord; MEDLINE=99416011; PubMed=10486557; [NCBI, ExPASy, EBI, Israel, Japan] Coulouarn Y., Jegou S., Tostivint H., Vaudry H., Lihrmann I.; "Cloning, sequence analysis and tissue distribution of the mouse and rat urotensin II precursors."; FEBS Lett. 457:28-32(1999).	
Comments	
<ul style="list-style-type: none"><li>• <b>FUNCTION:</b> HIGHLY POTENT VASOCONSTRICTOR (BY SIMILARITY).</li><li>• <b>SUBCELLULAR LOCATION:</b> Secreted.</li><li>• <b>TISSUE SPECIFICITY:</b> BRAIN-SPECIFIC. PREDOMINANTLY EXPRESSED IN MOTONEURONS OF THE BRAINSTEM AND SPINAL CORD.</li><li>• <b>SIMILARITY:</b> BELONGS TO THE UROTENSIN 2 FAMILY.</li></ul>	
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Cross-references	

EMBL	AF172175; AAD55767.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
MGD	MGI:1346329; Uts2.
GeneLynx	UTS2; Mus musculus.
SOURCE	UTS2; Mus musculus.
Ensembl	Q9QZQ3; Mus musculus. [Entry / Contig view]
InterPro	IPR001483; Urotensin_II. Graphical view of domain structure.
Pfam	PF02083; Urotensin_II; 1.
PROSITE	PS00984; UROTENSIN_II; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain].
BLOCKS	Q9QZQ3.
ProtoNet	Q9QZQ3.
ProtoMap	Q9QZQ3.
PRESAGE	Q9QZQ3.
DIP	Q9QZQ3.
ModBase	Q9QZQ3.
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Keywords

Hormone; Cleavage on pair of basic residues; Signal.

Features

Key	From	To	Length	Description	
SIGNAL	1	20	20	POTENTIAL.	<div> Feature aligner</div> <div> Feature table viewer</div>
PROPEP	21	104	84	POTENTIAL.	
PEPTIDE	110	123	14	UROTENSIN II.	
DISULFID	117	122		BY SIMILARITY.	


Sequence information

Length: 123 AA [This is the length of the unprocessed precursor]	Molecular weight: 13625 Da [This is the MW of the unprocessed precursor]	CRC64: F96486195137F7F4 [This is a checksum on the sequence]
<div><div>102030405060</div><div>MDRVPFCCLLFIGLLNPLLSLPVTDTGERTLQLPVLEEDALRALEELERMALLQTLRQTM</div><div>708090100110120</div><div>GTEAGESPGEAGPSTETPTPRGSMRKAFAGQNSNTVLSRLLARTRKQHKQHGAAPCECFWK</div></div> <div>YCI</div> <div>Q9QZQ3 in FASTA format</div>		


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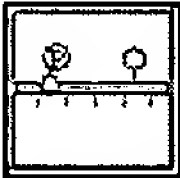
General information about the entry	
Entry name	UR2_RAT
Primary accession number	Q9QZQ4
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 40, October 2001
Sequence was last modified in	Release 40, October 2001
Annotations were last modified in	Release 40, October 2001
Name and origin of the protein	
Protein name	Urotensin II [Precursor]
Synonyms	U-II UII
Gene name	UTS2
From	<a href="#">Rattus norvegicus (Rat)</a> [TaxID: <a href="#">10116</a> ]
Taxonomy	<a href="#">Eukaryota</a> ; <a href="#">Metazoa</a> ; <a href="#">Chordata</a> ; <a href="#">Craniata</a> ; <a href="#">Vertebrata</a> ; <a href="#">Euteleostomi</a> ; <a href="#">Mammalia</a> ; <a href="#">Eutheria</a> ; <a href="#">Rodentia</a> ; <a href="#">Sciurognathi</a> ; <a href="#">Muridae</a> ; <a href="#">Murinae</a> ; <a href="#">Rattus</a> .
References	
[1] SEQUENCE FROM NUCLEIC ACID. TISSUE=Spinal cord; MEDLINE=99416011; PubMed=10486557; [ <a href="#">NCBI</a> , <a href="#">ExPASy</a> , <a href="#">EBI</a> , <a href="#">Israel</a> , <a href="#">Japan</a> ] <a href="#">Coulouarn Y.</a> , <a href="#">Jegou S.</a> , <a href="#">Tostivint H.</a> , <a href="#">Vaudry H.</a> , <a href="#">Lihrmann I.</a> ; "Cloning, sequence analysis and tissue distribution of the mouse and rat urotensin II precursors."; FEBS Lett. 457:28-32(1999).	
Comments	
<ul style="list-style-type: none"><li>• <b>FUNCTION:</b> HIGHLY POTENT VASOCONSTRICTOR (BY SIMILARITY).</li><li>• <b>SUBCELLULAR LOCATION:</b> Secreted.</li><li>• <b>TISSUE SPECIFICITY:</b> Brain-specific.</li><li>• <b>SIMILARITY:</b> BELONGS TO THE UROTENSIN 2 FAMILY.</li></ul>	
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Cross-references	

EMBL	AF172174; AAD55766.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
InterPro	IPR001483; Urotensin_II. <a href="#">Graphical view of domain structure.</a>
Pfam	PF02083; Urotensin_II; 1.
PROSITE	PS00984; UROTENSIN_II; 1.
ProDom	[ <a href="#">Domain structure</a> / <a href="#">List of seq. sharing at least 1 domain</a> ].
BLOCKS	<a href="#">Q9QZQ4</a> .
ProtoNet	<a href="#">Q9QZQ4</a> .
ProtoMap	<a href="#">Q9QZQ4</a> .
PRESAGE	<a href="#">Q9QZQ4</a> .
DIP	<a href="#">Q9QZQ4</a> .
ModBase	<a href="#">Q9QZQ4</a> .
SWISS-2DPAGE	<a href="#">Get region on 2D PAGE</a> .

Keywords

Hormone; Cleavage on pair of basic residues; Signal.

Features

Key	From	To	Length	Description	
SIGNAL	1	20	20	POTENTIAL.	 <a href="#">Feature aligner</a>
PROPEP	21	104	84	POTENTIAL.	
PEPTIDE	110	123	14	UROTENSIN II.	
DISULFID	117	122		BY SIMILARITY.	 <a href="#">Feature table viewer</a>

Sequence information

Length: 123 AA [This is the length of the unprocessed precursor]		Molecular weight: 13614 Da [This is the MW of the unprocessed precursor]		CRC64: E4F1A8EE124AF1EA [This is a checksum on the sequence]	
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MDRVPFCCLL	FVGLLNPLLS	FPVTDTGEMS	LQLPVLEENA	LRALEELERT	ALLQTLRQTV
70	80	90	100	110	120
GTEAEGSLGQ	ADPSAETPTP	RGSLRKALTG	QDSNTVLSRL	LARTRKQRKQ	HGTAPECFWK
YCI					
Q9QZQ4 in FASTA format					

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### General information about the entry

Entry name	UR2_HUMAN
Primary accession number	O95399
Secondary accession number	Q9UKP7
Entered in Swiss-Prot in	Release 40, October 2001
Sequence was last modified in	Release 40, October 2001
Annotations were last modified in	Release 41, February 2003

### Name and origin of the protein

Protein name	Urotensin II [Precursor]
Synonyms	U-II UII
Gene name	UTS2
From	<a href="#">Homo sapiens (Human)</a> [TaxID: 9606]
Taxonomy	<a href="#">Eukaryota</a> ; <a href="#">Metazoa</a> ; <a href="#">Chordata</a> ; <a href="#">Craniata</a> ; <a href="#">Vertebrata</a> ; <a href="#">Euteleostomi</a> ; <a href="#">Mammalia</a> ; <a href="#">Eutheria</a> ; <a href="#">Primates</a> ; <a href="#">Catarrhini</a> ; <a href="#">Hominidae</a> ; <a href="#">Homo</a> .

### References

#### [1] SEQUENCE FROM NUCLEIC ACID.

TISSUE=[Spinal cord](#);

MEDLINE=99080095; PubMed=9861051; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

[Coulouarn Y.](#), [Lihrmann I.](#), [Jegou S.](#), [Anouar Y.](#), [Tostivint H.](#), [Beauvillain J.C.](#), [Conlon J.M.](#), [Bern H.A.](#), [Vaudry H.](#);  
"Cloning of the cDNA encoding the urotensin II precursor in frog and human reveals intense expression of the urotensin II gene in motoneurons of the spinal cord.";

[Proc. Natl. Acad. Sci. U.S.A.](#) 95:15803-15808(1998).

#### [2] SEQUENCE FROM NUCLEIC ACID.

MEDLINE=99427933; PubMed=10499587; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

[Ames R.S.](#), [Sarau H.M.](#), [Chambers J.K.](#), [Willette R.N.](#), [Aiyar N.V.](#), [Romanic A.M.](#), [Louden C.S.](#), [Foley J.J.](#), [Sauermelch C.F.](#), [Coatney R.W.](#), [Ao Z.](#), [Disa J.](#), [Holmes S.D.](#), [Stadel J.M.](#), [Martin J.D.](#), [Liu W.-S.](#), [Glover G.I.](#), [Wilson S.](#), [McNulty D.E.](#), [Ellis C.E.](#), [Elshourbagy N.A.](#), [Shabon U.](#), [Trill J.J.](#), [Hay D.W.P.](#), [Ohlstein E.H.](#), [Bergsma D.J.](#), [Douglas S.A.](#);

"Human urotensin-II is a potent vasoconstrictor and agonist for the orphan receptor GPR14.";

[Nature](#) 401:282-286(1999).

#### [3] SEQUENCE FROM NUCLEIC ACID.

[Pearce A.](#);

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

### Comments

- **FUNCTION:** HIGHLY POTENT VASOCONSTRICTOR.
- **SUBCELLULAR LOCATION:** Secreted.
- **TISSUE SPECIFICITY:** Brain-specific.
- **SIMILARITY:** BELONGS TO THE UROTENSIN 2 FAMILY.

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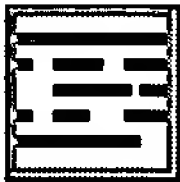
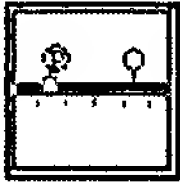
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Cross-references	
EMBL	AF104118; AAD13070.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AF140630; AAD55577.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] Z98884; CAB63148.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
Genew	HGNC:12636; UTS2.
CleanEx	HGNC:12636; UTS2.
MIM	604097 [NCBI / EBI].
GeneCards	UTS2.
GeneLynx	UTS2; Homo sapiens.
SOURCE	UTS2; Homo sapiens.
Ensembl	O95399; Homo sapiens. [Entry / Contig view]
InterPro	IPR001483; Urotensin_II. Graphical view of domain structure.
Pfam	PF02083; Urotensin_II; 1.
PROSITE	PS00984; UROTENSIN_II; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain].
BLOCKS	O95399.
ProtoNet	O95399.
ProtoMap	O95399.
PRESAGE	O95399.
DIP	O95399.
ModBase	O95399.
SWISS-2DPAGE	Get region on 2D PAGE.

Keywords
Hormone; Cleavage on pair of basic residues; Signal.

Features					
Key	From	To	Length	Description	
SIGNAL	1	20	20	POTENTIAL.	 <a href="#">Feature aligner</a>  <a href="#">Feature table viewer</a>
PROPEP	21	110	90		
PEPTIDE	114	124	11	UROTENSIN II.	
DISULFID	118	123		BY SIMILARITY.	
CONFLICT	1	19		MYKLASCCLLFIGFLNPLL -> METNVFHLMLCVTSARTH KSTSLCFGHFNSYP (IN REF. 2).	
CONFLICT	24	27		LDSR -> IHDLLL (IN REF. 2).	

Sequence information	
Length: 124 AA [This is the length of the unprocessed precursor]    Molecular weight: 14295 Da [This is the MW of the unprocessed precursor]    CRC64: C7A5FC7EFE00D312 [This is a checksum on the sequence]	
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General information about the entry	
Entry name	UR2R_RAT
Primary accession number	P49684
Secondary accession number	P48041
Entered in Swiss-Prot in	Release 33, February 1996
Sequence was last modified in	Release 38, July 1999
Annotations were last modified in	Release 41, February 2003
Name and origin of the protein	
Protein name	Urotensin II receptor
Synonyms	UR-II-R G protein-coupled sensory epithelial neuropeptide-like receptor SENR
Gene name	GPR14
From	<u>Rattus norvegicus (Rat)</u> [TaxID: <a href="#">10116</a> ]
Taxonomy	<u>Eukaryota</u> ; <u>Metazoa</u> ; <u>Chordata</u> ; <u>Craniata</u> ; <u>Vertebrata</u> ; <u>Euteleostomi</u> ; <u>Mammalia</u> ; <u>Eutheria</u> ; <u>Rodentia</u> ; <u>Sciurognathi</u> ; <u>Muridae</u> ; <u>Murinae</u> ; <u>Rattus</u> .
References	
[1] SEQUENCE FROM NUCLEIC ACID. MEDLINE=96115583; PubMed=8666380; [ <a href="#">NCBI</a> , <a href="#">ExPASy</a> , <a href="#">EBI</a> , <a href="#">Israel</a> , <a href="#">Japan</a> ] <a href="#">Marchese A.</a> , <a href="#">Heiber M.</a> , <a href="#">Nguyen T.</a> , <a href="#">Heng H.H.Q.</a> , <a href="#">Saldivia V.R.</a> , <a href="#">Cheng R.</a> , <a href="#">Murphy P.M.</a> , <a href="#">Tsui L.-C.</a> , <a href="#">Shi X.</a> , <a href="#">Gregor P.</a> , <a href="#">George S.R.</a> , <a href="#">O'Dowd B.F.</a> , <a href="#">Docherty J.M.</a> ; "Cloning and chromosomal mapping of three novel genes, GPR9, GPR10, and GPR14, encoding receptors related to interleukin 8, neuropeptide Y, and somatostatin receptors."; <a href="#">Genomics 29:335-344(1995)</a> .	
[2] SEQUENCE FROM NUCLEIC ACID. TISSUE= <a href="#">Circumvallate papillae</a> ; STRAIN= <a href="#">Sprague-Dawley</a> ; MEDLINE=95251679; PubMed=7733947; [ <a href="#">NCBI</a> , <a href="#">ExPASy</a> , <a href="#">EBI</a> , <a href="#">Israel</a> , <a href="#">Japan</a> ] <a href="#">Tal M.</a> , <a href="#">Ammar D.A.</a> , <a href="#">Karpuz M.</a> , <a href="#">Krizhanovsky V.</a> , <a href="#">Naim M.</a> , <a href="#">Thompson D.A.</a> ; "A novel putative neuropeptide receptor expressed in neural tissue, including sensory epithelia."; <a href="#">Biochem. Biophys. Res. Commun. 209:752-759(1995)</a> .	
[3] SEQUENCE FROM NUCLEIC ACID. TISSUE= <a href="#">Urinary bladder</a> ; STRAIN= <a href="#">Wistar</a> ; <a href="#">Suga H.</a> , <a href="#">Takao K.</a> ; "Expression of the rat SENR in the urinary bladder tissues."; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.	
[4] SEQUENCE FROM NUCLEIC ACID. TISSUE= <a href="#">Pheochromocytoma</a> ; <a href="#">Liu H.</a> , <a href="#">Zou M.</a> , <a href="#">Suga H.</a> , <a href="#">Takao K.</a> ; "The SENR/GPR14 expresses in rat pheochromocytoma PC 12 cells."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.	

Comments

- **FUNCTION:** HIGH AFINITY RECEPTOR FOR UROTENSIN II. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM (*BY SIMILARITY*).
- **SUBCELLULAR LOCATION:** Integral membrane protein.
- **TISSUE SPECIFICITY:** PREFERENTIALLY EXPRESSED IN NEURAL AND SENSORY TISSUES.
- **SIMILARITY:** BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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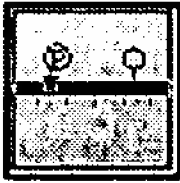
Cross-references

EMBL	U32673; AAC52593.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	U23483; AAA80111.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AB012210; BAA25251.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AB029611; BAA82357.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
InterPro	IPR000276; GPCR_Rhodpsn. Graphical view of domain structure.
Pfam	PF00001; 7tm_1; 1.
PRINTS	PR00237; GPCRRHODOPSN.
PROSITE	PS00237; G_PROTEIN_RECEP_F1_1; 1. PS50262; G_PROTEIN_RECEP_F1_2; 1.
GPCRDB	P49684; UR2R_RAT.
GPCRDB-Snakes	P49684.
ProDom	[Domain structure / List of seq. sharing at least 1 domain].
BLOCKS	P49684.
ProtoNet	P49684.
ProtoMap	P49684.
PRESAGE	P49684.
DIP	P49684.
ModBase	P49684.
SWISS-2DPAGE	Get region on 2D PAGE.

Keywords

G-protein coupled receptor; Transmembrane; Glycoprotein.

Features

Key	From	To	Length	Description	
DOMAIN	1	54	54	EXTRACELLULAR (POTENTIAL) .	
TRANSMEM	55	77	23	1 (POTENTIAL) .	
DOMAIN	78	87	10	CYTOPLASMIC (POTENTIAL) .	
TRANSMEM	88	113	26	2 (POTENTIAL) .	
DOMAIN	114	124	11	EXTRACELLULAR (POTENTIAL) .	
TRANSMEM	125	146	22	3 (POTENTIAL) .	
DOMAIN	147	167	21	CYTOPLASMIC (POTENTIAL) .	
TRANSMEM	168	186	19	4 (POTENTIAL) .	
DOMAIN	187	209	23	EXTRACELLULAR (POTENTIAL) .	<a href="#">Feature aligner</a>
TRANSMEM	210	232	23	5 (POTENTIAL) .	
DOMAIN	233	258	26	CYTOPLASMIC (POTENTIAL) .	
TRANSMEM	259	284	26	6 (POTENTIAL) .	
DOMAIN	285	299	15	EXTRACELLULAR (POTENTIAL) .	<a href="#">Feature table viewer</a>
TRANSMEM	300	321	22	7 (POTENTIAL) .	
DOMAIN	322	386	65	CYTOPLASMIC (POTENTIAL) .	
CARBOHYD	29	29		N-LINKED (GLCNAC...) (POTENTIAL) .	
CARBOHYD	33	33		N-LINKED (GLCNAC...) (POTENTIAL) .	
DISULFID	123	199		BY SIMILARITY.	
CONFLICT	315	315		F -> L (IN REF. 1) .	

Sequence information

Length: 386 AA   Molecular weight: 42707 Da   CRC64: FA4E95CC6A4CA27C [This is a checksum on the sequence]

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130	140	150	160	170	180
VGCRVLFSLD	FLTMHASIFT	LTIMSSERYA	AVLRPLDTVQ	RSKGYRKLLV	LGTWLLALLL
190	200	210	220	230	240
TLPMMLAIQL	VRRGSKSLCL	PAWGPRAHRT	YLTLFLFGTSI	VGPGLVIGLL	YVRLARAYWL
250	260	270	280	290	300
SQQASFQKTR	RLPNPRVLYL	ILGIVLLFWA	CFLPFWLWQL	LAQYHEAMPL	TPETARIVNY
310	320	330	340	350	360
LTTCCLTYGNS	CINPFLYTLL	TKNYREYLRG	RQRSLGSSCH	SPGSPGSFLP	SRVHLQQDSG
370	380				
RSLSSSSQQA	TETLMLSPVP	RNGALL			

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Hosted by NCSC US Mirror sites: <a href="#">Canada</a> <a href="#">China</a> <a href="#">Korea</a> <a href="#">Taiwan</a> <a href="#">USA</a>				
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## General information about the entry

Entry name	UR2R_HUMAN
Primary accession number	Q9UKP6
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 40, October 2001
Sequence was last modified in	Release 40, October 2001
Annotations were last modified in	Release 40, October 2001

## Name and origin of the protein

Protein name	Urotensin II receptor
Synonym	UR-II-R
Gene name	GPR14
From	<a href="#">Homo sapiens (Human)</a> [TaxID: 9606]
Taxonomy	<a href="#">Eukaryota</a> ; <a href="#">Metazoa</a> ; <a href="#">Chordata</a> ; <a href="#">Craniata</a> ; <a href="#">Vertebrata</a> ; <a href="#">Euteleostomi</a> ; <a href="#">Mammalia</a> ; <a href="#">Eutheria</a> ; <a href="#">Primates</a> ; <a href="#">Catarrhini</a> ; <a href="#">Hominidae</a> ; <a href="#">Homo</a> .

## References

[1] SEQUENCE FROM NUCLEIC ACID.  
MEDLINE=99427933; PubMed=10499587; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]  
[Ames R.S.](#), [Sarau H.M.](#), [Chambers J.K.](#), [Willette R.N.](#), [Aiyar N.V.](#), [Romanic A.M.](#), [Louden C.S.](#), [Foley J.J.](#), [Sauermelch C.F.](#), [Coatney R.W.](#), [Ao Z.](#), [Disa J.](#), [Holmes S.D.](#), [Stadel J.M.](#), [Martin J.D.](#), [Liu W.-S.](#), [Glover G.I.](#), [Wilson S.](#), [McNulty D.E.](#), [Ellis C.E.](#), [Elshourbagy N.A.](#), [Shabon U.](#), [Trill J.J.](#), [Hay D.W.P.](#), [Ohlstein E.H.](#), [Bergsma D.J.](#), [Douglas S.A.](#);  
"Human urotensin-II is a potent vasoconstrictor and agonist for the orphan receptor GPR14.";  
Nature 401:282-286(1999).

## Comments

- **FUNCTION:** HIGH AFINITY RECEPTOR FOR UROTENSIN II. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
- **SUBCELLULAR LOCATION:** Integral membrane protein.
- **TISSUE SPECIFICITY:** MOST ABUNDANT EXPRESSION IN THE HEART AND PANCREAS.
- **SIMILARITY:** BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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## Cross-references



EMBL	AF140631; AAD55578.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
Genew	HGNC:4468; GPR14.
CleanEx	HGNC:4468; GPR14.
MIM	600896 [NCBI / EBI].
GeneCards	GPR14.
GeneLynx	GPR14; Homo sapiens.
SOURCE	GPR14; Homo sapiens.
Ensembl	Q9UKP6; Homo sapiens. [Entry / Contig view]
InterPro	IPR000276; GPCR_Rhodpsn. Graphical view of domain structure.
Pfam	PF00001; 7tm_1; 1.
PRINTS	PR00237; GPCRRHODOPSN.
PROSITE	PS00237; G_PROTEIN_RECEP_F1_1; 1. PS50262; G_PROTEIN_RECEP_F1_2; 1.
GPCRDB	Q9UKP6; UR2R_HUMAN.
GPCRDB-Snakes	Q9UKP6.
ProDom	[Domain structure / List of seq. sharing at least 1 domain].
BLOCKS	Q9UKP6.
ProtoNet	Q9UKP6.
ProtoMap	Q9UKP6.
PRESAGE	Q9UKP6.
DIP	Q9UKP6.
ModBase	Q9UKP6.
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Keywords

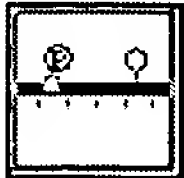
G-protein coupled receptor; Transmembrane; Glycoprotein.

Features

Key	From	To	Length	Description
DOMAIN	1	54	54	EXTRACELLULAR (POTENTIAL) .
TRANSMEM	55	77	23	1 (POTENTIAL) .
DOMAIN	78	87	10	CYTOPLASMIC (POTENTIAL) .
TRANSMEM	88	113	26	2 (POTENTIAL) .
DOMAIN	114	124	11	EXTRACELLULAR (POTENTIAL) .
TRANSMEM	125	146	22	3 (POTENTIAL) .
DOMAIN	147	167	21	CYTOPLASMIC (POTENTIAL) .
TRANSMEM	168	186	19	4 (POTENTIAL) .
DOMAIN	187	209	23	EXTRACELLULAR (POTENTIAL) .
TRANSMEM	210	232	23	5 (POTENTIAL) .
DOMAIN	233	258	26	CYTOPLASMIC (POTENTIAL) .
TRANSMEM	259	284	26	6 (POTENTIAL) .
DOMAIN	285	297	13	EXTRACELLULAR (POTENTIAL) .
TRANSMEM	298	318	21	7 (POTENTIAL) .
DOMAIN	319	389	71	CYTOPLASMIC (POTENTIAL) .
CARBOHYD	29	29		N-LINKED (GLCNAC...) (POTENTIAL) .
CARBOHYD	33	33		N-LINKED (GLCNAC...) (POTENTIAL) .
DISULFID	123	199		BY SIMILARITY.



Feature aligner



Feature table viewer

Sequence information

Length: 389 AA    Molecular weight: 42130 Da    CRC64: 6D6A88DBF78400CE [This is a checksum on the sequence]



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20

30

40

50

60

MALTPESPSSFPGLAATGSSVPEPPGGPNA

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80

90

100

110

120

MGVVGVGNA YTLVVTCRSLRAVASMYVYV

130

140

150

160

170

180

VGCRVLFGLD FLTMHASIFT LTVMSSERYA

190

200

210

220

230

240

TLPVMLAMRL VRRGPKSLCL PAWGPRAHRA

250

260

270

280

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300

SQRASFKRAR RPGARALRLV LGIVLLFWAC

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320

330

340

350

360

TCLTYGNSCA NPFLYTLLTR NYRDHLRGRV

370

380

SCSPQPTDSL VLAPAAPARP APEGPRAPA

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ScanProsite, MotifScan



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**General information about the entry**

Entry name	UR2R_BOVIN
Primary accession number	P49220
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 33, February 1996
Sequence was last modified in	Release 33, February 1996
Annotations were last modified in	Release 40, October 2001

**Name and origin of the protein**

Protein name	Urotensin II receptor [Fragment]
Synonyms	UR-II-R G protein-coupled sensory epithelial neuropeptide-like receptor SENR
Gene name	GPR14
From	<a href="#">Bos taurus (Bovine)</a> [TaxID: 9913]
Taxonomy	<a href="#">Eukaryota</a> ; <a href="#">Metazoa</a> ; <a href="#">Chordata</a> ; <a href="#">Craniata</a> ; <a href="#">Vertebrata</a> ; <a href="#">Euteleostomi</a> ; <a href="#">Mammalia</a> ; <a href="#">Eutheria</a> ; <a href="#">Cetartiodactyla</a> ; <a href="#">Ruminantia</a> ; <a href="#">Pecora</a> ; <a href="#">Bovoidea</a> ; <a href="#">Bovidae</a> ; <a href="#">Bovinae</a> ; <a href="#">Bos</a> .

**References**

[1] SEQUENCE FROM NUCLEIC ACID.  
TISSUE=[Retina](#);  
MEDLINE=95251679; PubMed=7733947; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]  
[Tal M.](#), [Ammar D.A.](#), [Karpuj M.](#), [Krizhanovsky V.](#), [Naim M.](#), [Thompson D.A.](#);  
"A novel putative neuropeptide receptor expressed in neural tissue, including sensory epithelia."  
[Biochem. Biophys. Res. Commun.](#) 209:752-759(1995).

**Comments**

- FUNCTION:** HIGH AFINITY RECEPTOR FOR UROTENSIN II. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM (BY SIMILARITY).
- SUBCELLULAR LOCATION:** Integral membrane protein.
- TISSUE SPECIFICITY:** EXPRESSED IN NEURAL TISSUE, INCLUDING SENSORY EPITHELIA.
- SIMILARITY:** BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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**Cross-references**

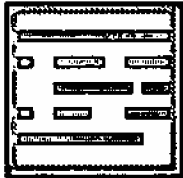
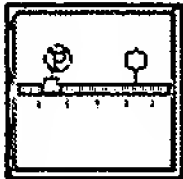
EMBL	U23459; AAC48464.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
InterPro	IPR000276; GPCR_Rhodpsn. <a href="#">Graphical view of domain structure.</a>
Pfam	PF00001; 7tm_1; 1.
PRINTS	PR00237; GPCRRHODOPSN.
PROSITE	PS00237; G_PROTEIN_RECEP_F1_1; PARTIAL. PS50262; G_PROTEIN_RECEP_F1_2; 1.
BLOCKS	P49220.
ProtoNet	P49220.
ProtoMap	P49220.
PRESAGE	P49220.
DIP	P49220.
ModBase	P49220.
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Keywords

G-protein coupled receptor; Transmembrane; Glycoprotein.

Features

Key	From	To	Length	Description
NON_TER	1	1		
TRANSMEM	<1	16	>16	2 (POTENTIAL) .
DOMAIN	17	27	11	EXTRACELLULAR (POTENTIAL) .
TRANSMEM	28	49	22	3 (POTENTIAL) .
DOMAIN	50	70	21	CYTOPLASMIC (POTENTIAL) .
TRANSMEM	71	89	19	4 (POTENTIAL) .
DOMAIN	90	111	22	EXTRACELLULAR (POTENTIAL) .
TRANSMEM	112	135	24	5 (POTENTIAL) .
DOMAIN	136	161	26	CYTOPLASMIC (POTENTIAL) .
TRANSMEM	162	187	26	6 (POTENTIAL) .
DOMAIN	188	194	7	EXTRACELLULAR (POTENTIAL) .
TRANSMEM	195	215	21	7 (POTENTIAL) .
DISULFID	26	102		POTENTIAL.
NON_TER	215	215		

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Sequence information

Length: 215 AA [This is the length of the partial sequence]		Molecular weight: 24575 Da [This is the MW of the partial sequence]		CRC64: 97F2D5041D96A624 [This is a checksum on the sequence]	
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70	80	90	100	110	120
TVQRSKGYRK	VLALGTWLLA	LLLALPMMLA	IRLVRRGHKS	LCLPAWGQRT	HRAYLTLLFG
130	140	150	160	170	180
TSIVGPGVVI	GLLYVRLARA	YWLSQRASFT	QTRRLPNPRV	LYLILGIVLL	FWACFLPFWL
190	200	210			
WQLLAQYRGA	PPLAPRSARI	VNYLTTCLTY	GNSCV		

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Sequence analysis tools: ProtParam, ProtScale, Compute  
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ScanProsite, MotifScan



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